

Filed on behalf of: Senior Party Genetics Institute, LLC

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UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE BOARD OF PATENT APPEALS  
AND INTERFERENCES

Stryker Corporation,  
Junior Party,  
(Patent 5,266,683,  
Inventors: Hermann Oppermann, Engin Ozkaynak, Thangavel Kuberasampath,  
David C. Rueger, Roy H.L. Pang),

v.

Genetics Institute, LLC,  
Senior Party,  
(Application 08/319,831,  
Inventors: Rodney M. Hewick, Jack H. Wang,  
John M. Wozney, Anthony J. Celeste).

Patent Interference 105,508 (RES)  
(Technology Center 1600)

GENETICS INSTITUTE CLEAN COPY OF CLAIMS

1 Pursuant to the Notice Declaring Interference dated October 6, 2006, Paper No. 1, the  
2 party Genetics Institute, LLC, submits a clean copy of its involved claims pending as of the time  
3 of the declaration of this interference.  
4  
5  
6

7 Respectfully submitted,  
8

9 Dated: October 20, 2006

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PATENT INTERFERENCE 105,508 (RES)

Genetics Institute, LLC,  
Senior Party,  
(Application 08/319,831,  
Inventors: Rodney M. Hewick, Jack H. Wang,  
John M. Wozney, Anthony J. Celeste).

CLEAN COPY OF CLAIMS

1. A purified BMP-8 protein characterized by:
  - (a) at least one of the following sequences:
    - i) Arg-His-Glu-Leu-Tyr-Val-Ser-Phe-Gln-Asp-Leu-Gly-Trp-Leu-Asp-Trp-Val-Ile-Ala-Pro-Gln-Gly-Tyr (SEQ ID NO: 1);
    - ii) Leu-Ser-Ala-Thr-Ser-Val-Leu-Tyr-Tyr-Asp-Ser-Ser-Asn-Asn-Val-Ile-Leu-Arg (SEQ ID NO: 2); and
    - iii) Ala-Cys-Cys-Ala-Pro-Thr-Lys (SEQ ID NO:3);
  - (b) a molecular weight of 28,000 - 38,000 daltons as determined by sodium dodecyl sulfate polyacrylamide gel electrophoresis; and
  - (c) a molecular weight of 14,000 - 20,000 daltons under reducing conditions as determined by sodium dodecyl sulfate polyacrylamide gel electrophoresis said protein being a disulfide linked dimer wherein each of the subunits contains the sequences set forth in part (a) and said protein having the ability to induce the formation of cartilage and/or bone.
26. A pharmaceutical formulation for bone and/or cartilage formation comprising an effective amount of a BMP-8 protein of claim 1 in a pharmaceutically acceptable vehicle.
27. A composition of claim 26 further comprising a matrix for supporting said composition and providing a surface for bone and/or cartilage formation.
28. The composition of claim 27 wherein said matrix comprises a material selected from the group consisting of hydroxyapatite, collagen, polylactic acid and tricalcium phosphate.
29. A pharmaceutical composition for wound healing and tissue repair said composition comprising an effective amount of a BMP-8 protein of claim 1 in a pharmaceutically acceptable vehicle.

## CERTIFICATE OF SERVICE

I hereby certify that a copy of the foregoing was served on the party Stryker Corporation through its attorney of record on this the 20<sup>th</sup> day of October, 2006 as follows:

## VIA FEDERAL EXPRESS

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Filed on behalf of: Stryker Corporation

Paper No. \_\_\_\_\_

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UNITED STATES PATENT AND TRADEMARK OFFICE

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BEFORE THE BOARD OF PATENT APPEALS  
AND INTERFERENCES

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**STRYKER CORPORATION,**

Junior Party

(Patent 5,266,683,

Inventors: Hermann Oppermann, Engin Ozkaynak, Thangavel Kuberasampath,  
David C. Rueger, Roy H.L. Pang),

v.

**GENETICS INSTITUTE, LLC,**

Senior Party

(Application 08/319,831,

Inventors: Rodney M. Hewick, Jack H. Wang,  
John M. Wozney, Anthony J. Celeste).

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Patent Interference No. 105,508 (RES)  
(Technology Center 1600)

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**STRYKER CORPORATION'S CLEAN COPY OF CLAIMS AND SEQUENCES**

STRYKER CORPORATION'S CLEAN COPY OF CLAIMS AND SEQUENCES

- 1 Pursuant to Bd. R. 110(a), Junior Party Stryker Corporation ("Stryker") submits the  
2 following clean copy of its involved claims of U.S. Patent 5,266,683. Junior Party Stryker also  
3 submits herewith a clean copy of the sequences recited in the involved claims.

21. An isolated protein comprising the amino acid sequence described by residues 306 to 402 of Seq. ID No. 28.
22. The protein of claim 21 comprising the amino acid sequence described by residues 270-402 of Seq. ID No. 28 (hOP2-Arg).
23. The protein of claim 22 comprising the amino acid sequence described by residues 267 to 402 of Seq. ID No. 28 (hOP2-Pro).
24. The protein of claim 23 comprising the amino acid sequence described by residues 264 to 402 of Seq. ID No. 28 (hOP2-Ala).
25. The protein of claim 24 comprising the amino acid sequence described by residues 243 to 402 of Seq. ID No. 28 (hOP2-Ser).
26. The protein of claim 25 comprising the amino acid sequence described by residues 1 to 402 of Seq. ID No. 28 (hOP2-PP).
27. The protein of claim 6, 15, 18 or 21 capable of inducing cartilage and bone formation when implanted in a mammal in association with a matrix.
28. Osteogenic protein expressed from recombinant DNA in a host cell,  
the protein comprising a pair of oxidized subunits disulfide bonded to  
produce a dimeric species, one of said subunits having an amino acid sequence  
sufficiently duplicative of the sequence comprising residues 335 to 431 of Seq. ID  
No. 1 (OPS),  
such that the disulfide bonded dimeric species comprising said subunit has  
a conformation capable of inducing cartilage and endochondral bone formation in  
a mammal when disposed within a matrix implanted in said mammal.
29. Osteogenic protein expressed from recombinant DNA in a host cell,

the protein comprising a pair of oxidized subunits disulfide bonded to produce a dimeric species, having a conformation capable of inducing cartilage and endochondral bone formation in a mammal when disposed within a matrix implanted in said mammal,

one of said subunits having an amino acid sequence encoded by a nucleic acid capable of hybridizing to a nucleic acid encoding OPS (res. 335-431, Seq. ID No. 1) under stringent hybridization conditions.

39. The protein of claim 28 or 29 wherein said subunit comprises at least the osteogenically active region of a protein selected from the group consisting of: mOP1-PP (residues 1-430, Seq. ID No. 24); mOP2-PP (residues 1-399 of Seq. ID No. 26); and hOP2-PP (residues 1-402 of Seq. ID No. 28).
45. An isolated polypeptide chain useful as a subunit of a dimeric osteogenic protein, said polypeptide chain having an amino acid sequence sharing greater than 74% identity with the sequence described by residues 264-402 of Seq. ID No. 28 (hOP2-Ala) such that the disulfide bonded dimeric species comprising said polypeptide chain is capable of inducing endochondral bone formation when implanted in a mammal in association with a matrix.
46. An isolated polypeptide chain useful as a subunit of a dimeric osteogenic protein having a conformation capable of inducing endochondral bone formation in a mammal when implanted in a mammal in association with a matrix, said polypeptide chain having an amino acid sequence encoded by a nucleic acid capable of hybridizing to a nucleic acid encoding the pro region of mOP2-PP (res. 17-260 of Seq. ID No. 26) or hOP2-PP (res. 17-263 of Seq. ID No. 28) under stringent hybridization conditions.
47. The polypeptide chain of claim 45 or 46 having an amino acid sequence sharing greater than 80% identity with the amino acid sequence of hOP2-Ala.



- 1           48.     The polypeptide chain of claim 47 having an amino acid sequence sharing greater  
2                 than 85% identity with the amino acid sequence of hOP2-Ala.  
3
- 4           49.     The polypeptide chain of claim 45 or 46 wherein said amino acid sequence is  
5                 selected from the group consisting of: mOP2-Ala (residues 261-399 Seq. ID No.  
6                 26); hOP2-Ala (residues 264-402 of Seq. ID No. 28); hOP2-Pro (residues 267-  
7                 402 of Seq. ID No. 28); hOP2-Arg (residues 270-402 of Seq. ID No. 28) and  
8                 hOP2-Ser (residues 243-402 of Seq. ID No. 28).  
9
- 10          50.     The polypeptide chain of claim 45 or 46 wherein said amino acid sequence is  
11                 derived from an amino acid sequence selected from the group consisting of:  
12                 mOP2-PP (residues 1-399 of Seq. ID No. 26) and hOP2-PP (residues 1-402 of  
13                 Seq. ID No. 28) including allelic variants thereof, and natural and biosynthetic  
14                 mutants thereof.  
15
- 16          51.     The polypeptide chain of claim 45 or 46 that is glycosylated.  
17
- 18          52.     An isolated dimeric protein capable of inducing cartilage or endochondral bone  
19                 formation in a mammal when implanted in said mammal in association with a  
20                 matrix,  
21                         said protein comprising a pair of disulfide-bonded polypeptide chains  
22                 constituting a dimeric species, wherein each said polypeptide chain is the  
23                 polypeptide chain of claim 45 or 46.  
24
- 25          53.     The dimeric protein of claim 52 wherein each said polypeptide chain is  
26                 independently selected and comprises at least the osteogenically active region of  
27                 mOP2-PP (residues 1-399 of Seq. ID No. 26) or hOP2-PP (residues 1-402 of Seq.  
28                 ID No. 28).  
29
- 30          54.     The dimeric protein of claim 53, wherein each said polypeptide chain is  
31                 independently selected from the group consisting of: mOP2-Ala (residues 261-  
32                 399 Seq. ID No. 26); hOP2-Ala (residues 264-402 of Seq. ID No. 28); hOP2-Pro

(residues 267-402 of Seq. ID No. 28); hOP2-Arg (residues 270-402 of Seq. ID No. 28) and hOP2-Ser (residues 243-402 of Seq. ID No. 28).

58. A protein expressed from recombinant DNA in a host cell, said protein comprising an amino acid sequence encoded by a nucleic acid capable of hybridizing to a nucleic acid encoding residues 306-402 of hOP2 (Seq. ID No. 28) under stringent hybridization conditions.

Interference No. 105,508 (RES)  
**STRYKER CORPORATION v. GENETICS INSTITUTE, LLC**

**SEQUENCE DESCRIPTION: SEQ ID NO:1:**

5	GGTGGCGGCC CGAGAGCCCGG AGCCCGGGTA GCGCGTAGAG CCGGCGCG ATG CAC GTG	57
6		Met His Val
7		1
9	CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA	105
10	Arg Ser Leu Arg Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala	
11	5 10 15	
13	CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC	153
14	Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn	
15	20 25 30 35	
17	GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG	201
18	Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg	
19	40 45 50	
21	CGG GAG ATG CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC	249
22	Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg	
23	55 60 65	
25	CCG CGC CCG CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG	297
26	Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met	
27	70 75 80	
29	CTG GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG GGC GGC GGG CCC GGC	345
30	Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly	
31	85 90 95	
33	GGC CAG GGC TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC	393
34	Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly	
35	100 105 110 115	
37	CCC CCT CTG GCC AGC CTG CAA GAT AGC CAT TTC CTC ACC GAC GCC GAC	441
38	Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp	
39	120 125 130	
41	ATG GTC ATG AGC TTC GTC AAC CTC GTG GAA CAT GAC AAG GAA TTC TTC	489
42	Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Leu Phe Phe	
43	135 140 145	
45	CAC CCA CGC TAC CAC CAT CGA GAG TTC CGG TTT GAT CTT TCC AAG ATC	537
46	His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile	
47	150 155 160	
49	CCA GAA GGC GAA GCT GTC ACG GCA GCC GAA TTC CGG ATC TAC AAG GAC	585
50	Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp	
51	165 170 175	
53	TAC ATC CGG GAA CGC TTC GAC AAT GAG ACG TTC CGG ATC AGC GTT TAT	633
54	Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr	
55	180 185 190 195	
57	CAG GTG CTC CAG GAG CAC TTG GGC AGG GAA TCG GAT CTC TTC CTG CTC	681

## STRYKER CORPORATION v. GENETICS INSTITUTE, LLC

1	Gln	Val	Leu	Gln	Glu	His	Leu	Gly	Arg	Glu	Ser	Asp	Leu	Phe	Leu	Leu	
2					200					205					210		
3																	
4	GAC	AGC	CGT	ACC	CTC	TGG	GCC	TCG	GAG	GAG	GGC	TGG	CTG	GTG	TTT	GAC	729
5	Asp	Ser	Arg	Thr	Leu	Trp	Ala	Ser	Glu	Glu	Gly	Trp	Leu	Val	Phe	Asp	
6				215					220				225				
7																	
8	ATC	ACA	GCC	ACC	AGC	AAC	CAC	TGG	GTG	GTC	AAT	CCG	CGG	CAC	AAC	CTG	777
9	Ile	Thr	Ala	Thr	Ser	Asn	His	Trp	Val	Val	Asn	Pro	Arg	His	Asn	Leu	
10			230					235					240				
11																	
12	GGC	CTG	CAG	CTC	TCG	GTG	GAG	ACG	CTG	GAT	GGG	CAG	AGC	ATC	AAC	CCC	825
13	Gly	Leu	Gln	Leu	Ser	Val	Glu	Thr	Leu	Asp	Gly	Gln	Ser	Ile	Asn	Pro	
14			245				250					255					
15																	
16	AAG	TTG	GCG	GGC	CTG	ATT	GGG	CGG	CAC	GGG	CCC	CAG	AAC	AAG	CAG	CCC	873
17	Lys	Leu	Ala	Gly	Leu	Ile	Gly	Arg	His	Gly	Pro	Gln	Asn	Lys	Gln	Pro	
18		260				265					270				275		
19																	
20	TTC	ATG	GTG	GCT	TTC	TTC	AAG	GCC	ACG	GAG	GTC	CAC	TTC	CGC	AGC	ATC	921
21	Phe	Met	Val	Ala	Phe	Phe	Lys	Ala	Thr	Glu	Val	His	Phe	Arg	Ser	Ile	
22					280					285				290			
23																	
24	CGG	TCC	ACG	GGG	AGC	AAA	CAG	CGC	AGC	CAG	AAC	CGC	TCC	AAG	ACG	CCC	969
25	Arg	Ser	Thr	Gly	Ser	Lys	Gln	Arg	Ser	Gln	Asn	Arg	Ser	Lys	Thr	Pro	
26				295				300					305				
27																	
28	AAG	AAC	CAG	GAA	GCC	CTG	CGG	ATG	GCC	AAC	GTG	GCA	GAG	AAC	AGC	AGC	1017
29	Lys	Asn	Gln	Glu	Ala	Leu	Arg	Met	Ala	Asn	Val	Ala	Glu	Asn	Ser	Ser	
30			310					315				320					
31																	
32	AGC	GAC	CAG	AGG	CAG	GCC	TGT	AAG	AAG	CAC	GAG	CTG	TAT	GTC	AGC	TTC	1065
33	Ser	Asp	Gln	Arg	Gln	Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	
34		325					330					335					
35																	
36	CGA	GAC	CTG	GGC	TGG	CAG	GAC	TGG	ATC	ATC	GCG	CCT	GAA	GGC	TAC	GCC	1113
37	Arg	Asp	Leu	Gly	Trp	Gln	Asp	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala	
38		340			345					350				355			
39																	
40	GCC	TAC	TAC	TGT	GAG	GGG	GAG	TGT	GCC	TTC	CCT	CTG	AAC	TCC	TAC	ATG	1161
41	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala	Phe	Pro	Leu	Asn	Ser	Tyr	Met	
42					360				365					370			
43																	
44	AAC	GCC	ACC	AAC	CAC	GCC	ATC	GTG	CAG	ACG	CTG	GTC	CAC	TTC	ATC	AAC	1209
45	Asn	Ala	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu	Val	His	Phe	Ile	Asn	
46				375				380					385				
47																	
48	CCG	GAA	ACG	GTG	CCC	AAG	CCC	TGC	TGT	GCG	CCC	ACG	CAG	CTC	AAT	GCC	1257
49	Pro	Glu	Thr	Val	Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln	Leu	Asn	Ala	
50			390					395					400				
51																	
52	ATC	TCC	GTC	CTC	TAC	TTC	GAT	GAC	AGC	TCC	AAC	GTC	ATC	CTG	AAG	AAA	1305
53	Ile	Ser	Val	Leu	Tyr	Phe	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys	Lys	
54		405					410					415					
55																	
56	TAC	AGA	AAC	ATG	GTG	GTC	CGG	GCC	TGT	GGC	TGC	CAC	TAGCTCCTCC				1351
57	Tyr	Arg	Asn	Met	Val	Val	Arg	Ala	Cys	Gly	Cys	His					
58		420				425					430						

1  
 2 GAGAATTCAG ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTCG CCTTGGCCAG 1411  
 3  
 4 GAACCAGCAG ACCAACTGCC TTTTGTGAGA CCTTCCCTC CCTATCCCCA ACTTTAAAGG 1471  
 5  
 6 TGTGAGAGTA TTAGGAAACA TGAGCAGCAT ATGGCTTTTG ATCAGTTTTT CAGTGGCAGC 1531  
 7  
 8 ATCCAATGAA CAAGATCCTA CAAGCTGTGC AGGCCAAAACC TAGCAGGAAA AAAAAACAAC 1591  
 9  
 10 GCATAAAGAA AAATGGCCGG GCCAGTTCAT TGGCTGGGAA GTCTCAGCCA TGCACGGACT 1651  
 11  
 12 CGTTTCCAGA GGTAATTATG AGCGCCTACC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG 1711  
 13  
 14 GGCGTGGCAA GGGGTGGGCA CATTGGTGTG TGTGCGAAG GAAAATTGAC CCGGAAGTTC 1771  
 15  
 16 CTGTAATAAA TGTACAATA AACGAATGA ATGAAAAAAA AAAAAAAAAA A 1822  
 17  
 18  
 19  
 20

## SEQUENCE DESCRIPTION: SEQ ID NO:24:

21  
 22  
 23 CTGCAGCAAG TGACCTCGGG TCGTGGACCG CTGCCCTGCC CCTCCGCTG CCACCTGGGG 60  
 24  
 25 CGCGCGCGGG CCGGTGCCCC GGATCGCGCG TAGAGCCGGC GCG ATG CAC GTG CGC 115  
 26 Met His Val Arg  
 27 1  
 28  
 29 TCG CTG CGC GCT GCG GCG CCA CAC AGC TTC GTG GCG CTC TGG GCG CCT 163  
 30 Ser Leu Arg Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala Pro  
 31 5 10 15 20  
 32  
 33 CTG TTC TTG CTG CGC TCC GCC CTG GCC GAT TTC AGC CTG GAC AAC GAG 211  
 34 Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn Glu  
 35 25 30 35  
 36  
 37 GTG CAC TCC AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG CGG 259  
 38 Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg Arg  
 39 40 45 50  
 40  
 41 GAG ATG CAG CGG GAG ATC CTG TCC ATC TTA GGG TTG CCC CAT CGC CCG 307  
 42 Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg Pro  
 43 55 60 65  
 44  
 45 CGC CCG CAC CTC CAG GGA AAG CAT AAT TCG GCG CCC ATG TTC ATG TTG 355  
 46 Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met Leu  
 47 70 75 80  
 48  
 49 GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG AGC GGG CCG GAC GGA CAG 403  
 50 Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Ser Gly Pro Asp Gly Gln  
 51 85 90 95 100  
 52  
 53 GGC TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC CCC CCT 451  
 54 Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly Pro Pro  
 55 105 110 115  
 56  
 57 TTA GCC AGC CTG CAG GAC AGC CAT TTC CTC ACT GAC GCC GAC ATG GTC 499  
 58 Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp Met Val

1																	
2																	
3	ATG	AGC	TTC	GTC	AAC	CTA	GTG	GAA	CAT	GAC	AAA	GAA	TTC	TTC	CAC	CCT	547
4	Met	Ser	Phe	Val	Asn	Leu	Val	Glu	His	Asp	Lys	Glu	Phe	Phe	His	Pro	
5			135					140					145				
6																	
7	CGA	TAC	CAC	CAT	CGG	GAG	TTC	CGG	TTT	GAT	CTT	TCC	AAG	ATC	CCC	GAG	595
8	Arg	Tyr	His	His	Arg	Glu	Phe	Arg	Phe	Asp	Leu	Ser	Lys	Ile	Pro	Glu	
9			150					155					160				
10																	
11	GGC	GAA	CGG	GTG	ACC	GCA	GCC	GAA	TTC	AGG	ATC	TAT	AAG	GAC	TAC	ATC	643
12	Gly	Glu	Arg	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	Lys	Asp	Tyr	Ile	
13			165				170				175					180	
14																	
15	CGG	GAG	CGA	TTT	GAC	AAC	GAG	ACC	TTC	CAG	ATC	ACA	GTC	TAT	CAG	GTG	691
16	Arg	Glu	Arg	Phe	Asp	Asn	Glu	Thr	Phe	Gln	Ile	Thr	Val	Tyr	Gln	Val	
17					185					190					195		
18																	
19	CTC	CAG	GAG	CAC	TCA	GGC	AGG	GAG	TCG	GAC	CTC	TTC	TTG	CTG	GAC	AGC	739
20	Leu	Gln	Glu	His	Ser	Gly	Arg	Glu	Ser	Asp	Leu	Phe	Leu	Leu	Asp	Ser	
21					200					205					210		
22																	
23	CGC	ACC	ATC	TGG	GCT	TCT	GAG	GAG	GGC	TGG	TTG	GTG	TTT	GAT	ATC	ACA	787
24	Arg	Thr	Ile	Trp	Ala	Ser	Glu	Glu	Gly	Trp	Leu	Val	Phe	Asp	Ile	Thr	
25				215					220					225			
26																	
27	GCC	ACC	AGC	AAC	CAC	TGG	GTG	GTC	AAC	CCT	CGG	CAC	AAC	CTG	GGC	TTA	835
28	Ala	Thr	Ser	Asn	His	Trp	Val	Val	Asn	Pro	Arg	His	Asn	Leu	Gly	Leu	
29			230						235				240				
30																	
31	CAG	CTC	TCT	GTG	GAG	ACC	CTG	GAT	GGG	CAG	AGC	ATC	AAC	CCC	AAG	TTG	883
32	Gln	Leu	Ser	Val	Glu	Thr	Leu	Asp	Gly	Gln	Ser	Ile	Asn	Pro	Lys	Leu	
33			245				250				255					260	
34																	
35	GCA	GGC	CTG	ATT	GGA	CGG	CAT	GGA	CCC	CAG	AAC	AAG	CAA	CCC	TTC	ATG	931
36	Ala	Gly	Leu	Ile	Gly	Arg	His	Gly	Pro	Gln	Asn	Lys	Gln	Pro	Phe	Met	
37					265					270					275		
38																	
39	GTG	GCC	TTC	TTC	AAG	GCC	ACG	GAA	GTC	CAT	CTC	CGT	AGT	ATC	CGG	TCC	979
40	Val	Ala	Phe	Phe	Lys	Ala	Thr	Glu	Val	His	Leu	Arg	Ser	Ile	Arg	Ser	
41					280					285					290		
42																	
43	ACG	GGG	GGC	AAG	CAG	CGC	AGC	CAG	AAT	CGC	TCC	AAG	ACG	CCA	AAG	AAC	1027
44	Thr	Gly	Gly	Lys	Gln	Arg	Ser	Gln	Asn	Arg	Ser	Lys	Thr	Pro	Lys	Asn	
45			295						300				305				
46																	
47	CAA	GAG	GCC	CTG	AGG	ATG	GCC	AGT	GTG	GCA	GAA	AAC	AGC	AGC	AGT	GAC	1075
48	Gln	Glu	Ala	Leu	Arg	Met	Ala	Ser	Val	Ala	Glu	Asn	Ser	Ser	Ser	Asp	
49			310					315				320					
50																	
51	CAG	AGG	CAG	GCC	TGC	AAG	AAA	CAT	GAG	CTG	TAC	GTC	AGC	TTC	CGA	GAC	1123
52	Gln	Arg	Gln	Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	Arg	Asp	
53			325				330				335					340	
54																	
55	CTT	GGC	TGG	CAG	GAC	TGG	ATC	ATT	GCA	CCT	GAA	GGC	TAT	GCT	GCC	TAC	1171
56	Leu	Gly	Trp	Gln	Asp	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala	Ala	Tyr	
57					345					350					355		
58																	

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1	TAC TGT GAG GGA GAG TGC GCC TTC CCT CTG AAC TCC TAC ATG AAC GCC	1219
2	Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala	
3	360 365 370	
4		
5	ACC AAC CAC GCC ATC GTC CAG ACA CTG GTT CAC TTC ATC AAC CCA GAC	1267
6	Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Asp	
7	375 380 385	
8		
9	ACA GTA CCC AAG CCC TGC TGT GCG CCC ACC CAG CTC AAC GCC ATC TCT	1315
10	Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser	
11	390 395 400	
12		
13	GTC CTC TAC TTC GAC GAC AGC TCT AAT GTC ATC CTG AAG AAG TAC AGA	1363
14	Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg	
15	405 410 415 420	
16		
17	AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCTTCC TGAGACCCGTG	1413
18	Asn Met Val Val Arg Ala Cys Gly Cys His	
19	425 430	
20		
21	ACCTTTGCGG GGCCACACCT TTCCAAATCT TCGATGTCTC ACCATCTAAG TCTCTCACTG	1473
22		
23	CCCACCTTGG CGAGGAGAAC AGACCAACCT CTCCTGAGCC TTCCCTCACC TCCCAACCGG	1533
24		
25	AAGCATGTAA GGGTTCCAGA AACCTGAGCG TGCAGCAGCT GATGAGCGCC CTTTCTCTCT	1593
26		
27	GGCAGCTGAC GGACAAGATC CTACCAGCTA CCACAGCAAA CGCCTAAGAG CAGGAAAAAT	1653
28		
29	GTCTGCCAGG AAAGTGTCCA GTGTCCACAT GGCCCTTGCG GCTCTGAGTC TTTGAGGAGT	1713
30		
31	AATCGCAAGC CTCGTTTCAGC TGCAGCAGAA GGAAGGGCTT AGCCAGGGGTG GGCCTGGCG	1773
32		
33	TCTGTGTTGA AGGGAACCA AGCAGAAGCC ACTGTAATGA TATGTCACAA TAAAACCCAT	1833
34		
35	GAATGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAGAATTG	1873
36		
37		
38		
39		
40	SEQUENCE DESCRIPTION: SEQ ID NO:26:	
41		
42	gaattccgct gccaggcaca ggtgcgccgt ctggctctcc ccgtctggcg tcagccgagc	60
43		
44	ccgaccagct accagtggaat gcgcgcgcgc tgaaagtcag ag atg gct atg cgt	114
45	Met Ala Met Arg	
46	1	
47		
48	ccc ggg cca ctc tgg cta ttg ggc ctt gct ctg tgc gcg ctg gga ggc	162
49	Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys Ala Leu Gly Gly	
50	5 10 15 20	
51		
52	ggc cac ggt ccc ggt ccc ccg cac acc tgt ccc cag cgt cgc ctg gga	210
53	Gly His Gly Pro Gly Pro Pro His Thr Cys Pro Gln Arg Arg Leu Gly	
54	25 30 35	
55		
56	gcg cgc gac cgg gac atg cag cgt gaa atc ctg ccg gtg ctc ggg cta	258
57	Ala Arg Asp Arg Asp Met Gln Arg Glu Ile Leu Pro Val Leu Gly Leu	
58	40 45 50	

- 11 -



1	Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp Gly His Gly Ser Arg Gly	
2	280 285 290	
3		
4	aga gag gtt tgc cgc agg cat gag ctc tac gtc aga ttc cgt gac ctt	1026
5	Arg Glu Val Cys Arg Arg His Glu Leu Tyr Val Arg Phe Arg Asp Leu	
6	295 300 305	
7		
8	ggc tgg ctg gac tgg gtc atc gcc ccc cag ggc tac tct gcc tat tac	1074
9	Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr	
10	310 315 320	
11		
12	tgt gag ggg gag tgt gct ttc cca ctg gac tcc tgt atg aac gcc acc	1122
13	Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp Ser Cys Met Asn Ala Thr	
14	325 330 335 340	
15		
16	aac cat gcc atc ttg cag tct ctg gtg cac ctg atg aag cca gat gtt	1170
17	Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro Asp Val	
18	345 350 355	
19		
20	gtc ccc aag gca tgc tgt gca ccc acc aaa ctg agt gcc acc tct gtg	1218
21	Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val	
22	360 365 370	
23		
24	ctg tac tat gac agc agc aac aat gtc atc ctg cgt aaa cac cgt aac	1266
25	Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn	
26	375 380 385	
27		
28	atg gtg gtc aag gcc tgt ggc tgc cac tgaggccccg cccagcatcc	1313
29	Met Val Val Lys Ala Cys Gly Cys His	
30	390 395	
31		
32	tgccttact acottacat ctggccgggc cccctctccag aggcagaaac ccttctatgt	1373
33		
34	tatcatagct cagacagggg caatggggagg cccttcaact cccctggcca ctctctgcta	1433
35		
36	aaattctggt ctttccagct tctctgtgct ttcattggggt ttccggggcta tcaccccgcc	1493
37		
38	ctctccatcc tctaccacca agcatagact gaatgcacac agcatccag agctatgcta	1553
39		
40	actgagaggt ctgggggtcag cactgaaggc ccacatgagg aagactgac cttggccatc	1613
41		
42	ctcagcccac aatggcaaat tctggatggt ctaagaagcc ctggaattct aaactagatg	1673
43		
44	atctgggctc tctgcacat tcaattgtggc agttgggaca tttttaggta taacagacac	1733
45		
46	atacacttag atcaatgcac cgctgtactc cttgaaatca gagctagctt gttagaaaaa	1793
47		
48	gaatcagagc caggatatgc ggtgcattgc attaatccca gcgctaaga gacagagaca	1853
49		
50	ggagaatctc tgtgagttca aggccacata gaaagagcct gtctcgggag caggaaaaaa	1913
51		
52	aaaaaaaaacg gaattc	1929
53		
54		
55		
56		
57	SEQUENCE DESCRIPTION: SEQ ID NO:28:	
58		

1	GGCGCCGCGCA	GAGCAGGAGT	GGCTGGAGGA	GCTGTGTTG	GAGCAGGAGG	TGGCACGCGCA	60
2							
3	GGGCTGGAGG	GCTCCCTATG	AGTGGCGGAG	ACGGCCGAGG	AGGCGCTGGA	GCAACAGCTC	120
4							
5	CCACACCGCA	CCAAGCGGTG	GCTGCAGGAG	CTCGCCCATC	GCCCTGCGCG	TGCTCGGACC	180
6							
7	GCGGCCACAG	CCGGACTGGC	GGGTACGGCG	GCGACAGAGG	CATTGGCCGA	GAGTCCAGT	240
8							
9	CCGCAGAGTA	GCCCCGGCCT	CGAGGCGGTG	GCGTCCCGGT	CCTCTCCGTC	CAGGAGCCAG	300
10							
11	GACAGGTGTC	GCGCGGCGGG	GCTCCAGGGA	CCGCGCCTGA	GGCCGGCTCG	CCGCCCGTCC	360
12							
13	CGCCCCCGCC	CGCCGCCCGC	CGCCCGCCGA	GCCCAAGCCTC	CTTGCCGTCG	GGGCGTCCCC	420
14							
15	AGGCCCTGGG	TCGGCCCGCG	AGCCGATGCG	CGCCCGCTGA	GCGCCCCAGC	TGAGCGCCCC	480
16							
17	CGGCCTGCC	ATG ACC GCG CTC CCC GGC CCG CTC TGG CTC CTG GGC CTG					528
18		Met Thr Ala Leu Pro Gly Pro Leu Trp Leu Leu Gly Leu					
19		1	5	10			
20							
21	GCG CTA TGC GCG CTG GGC	GGG GGC GGC CCC GGC CTG CGA CCC CCG CCC					576
22	Ala Leu Cys Ala Leu Gly	Gly Gly Gly Pro Gly Leu Arg Pro Pro Pro					
23	15	20	25				
24							
25	GGC TGT CCC CAG CGA CGT CTG GGC GCG CGC GAG CGC CGG GAC GTG CAG						624
26	Gly Cys Pro Gln Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Val Gln						
27	30	35	40	45			
28							
29	CGC GAG ATC CTG GCG GTG CTC GGG CTG CCT GGG CGG CCC CGG CCC CGC						672
30	Arg Glu Ile Leu Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg						
31		50	55	60			
32							
33	GCG CCA CCC GCC GCC TCC CGG CTG CCC GCG TCC GCG CCG CTC TTC ATG						720
34	Ala Pro Pro Ala Ala Ser Arg Leu Pro Ala Ser Ala Pro Leu Phe Met						
35	65	70	75				
36							
37	CTG GAC CTG TAC CAC GCC ATG GCC GGC GAC GAC GAC GAG GAC GGC GCG						768
38	Leu Asp Leu Tyr His Ala Met Ala Gly Asp Asp Asp Glu Asp Gly Ala						
39	80	85	90				
40							
41	CCC GCG GAG CGG CGC CTG GGC CGC GCC GAC CTG GTC ATG AGC TTC GTT						816
42	Pro Ala Glu Arg Arg Leu Gly Arg Ala Asp Leu Val Met Ser Phe Val						
43	95	100	105				
44							
45	AAC ATG GTG GAG CGA GAC CGT GCC CTG GGC CAC CAG GAG CCC CAT TGG						864
46	Asn Met Val Glu Arg Asp Arg Ala Leu Gly His Gln Glu Pro His Trp						
47	110	115	120	125			
48							
49	AAG GAG TTC CGC TTT GAC CTG ACC CAG ATC CCG GCT GGG GAG GCG GTC						912
50	Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val						
51	130	135	140				
52							
53	ACA GCT GCG GAG TTC CGG ATT TAC AAG GTG CCC AGC ATC CAC CTG CTC						960
54	Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val Pro Ser Ile His Leu Leu						
55	145	150	155				
56							
57	AAC AGG ACC CTC CAC GTC AGC ATG TTC CAG GTG GTC CAG GAG CAG TCC						1008
58	Asn Arg Thr Leu His Val Ser Met Phe Gln Val Val Gln Glu Gln Ser						

1	160	165	170	
2				
3	AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT CTT CAG ACG CTC CGA GCT			1056
4	Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln Thr Leu Arg Ala			
5	175	180	185	
6				
7	GGA GAC GAG GGC TGG CTG GTG CTG GAT GTC ACA GCA GCC AGT GAC TGC			1104
8	Gly Asp Glu Gly Trp Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys			
9	190	195	200	205
10				
11	TGG TTG CTG AAG CGT CAC AAG GAC CTG GGA CTC CGC CTC TAT GTG GAG			1152
12	Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu			
13	210	215	220	
14				
15	ACT GAG GAC GGG CAC AGC GTG GAT CCT GGC CTG GCC GGC CTG CTG GGT			1200
16	Thr Glu Asp Gly His Ser Val Asp Pro Gly Leu Ala Gly Leu Leu Gly			
17	225	230	235	
18				
19	CAA CGG GCC CCA CGC TCC CAA CAG CCT TTC GTG GTC ACT TTC TTC AGG			1248
20	Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val Thr Phe Phe Arg			
21	240	245	250	
22				
23	GCC AGT CCG AGT CCC ATC CGC ACC CCT CGG GCA GTG AGG CCA CTG AGG			1296
24	Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg Ala Val Arg Pro Leu Arg			
25	255	260	265	
26				
27	AGG AGS CAG CCG AAG AAA AGC AAC GAG CTG CCG CAG GCC AAC CGA CTC			1344
28	Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln Ala Asn Arg Leu			
29	270	275	280	285
30				
31	CCA GGG ATC TTT GAT GAC GTC CAC GGC TCC CAC GGC CGG CAG GTC TGC			1392
32	Pro Gly Ile Phe Asn Asp Val His Gly Ser His Gly Arg Gln Val Cys			
33	290	295	300	
34				
35	CGT CGG CAC GAG CTC TAC GTC AGC TTC CAG GAC CTC GGC TGG CTG GAC			1440
36	Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp			
37	305	310	315	
38				
39	TGG GTC ATC GCT CCC CAA GGC TAC TCG GCC TAT TAC TGT GAG GGG GAG			1488
40	Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu			
41	320	325	330	
42				
43	TGC TCC TTC CCA CTG GAC TCC TGC ATG AAT GCC ACC AAC CAC GCC ATC			1536
44	Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile			
45	335	340	345	
46				
47	CTG CAG TCC CTG GTG CAC CTG ATG AAG CCA AAC GCA GTC CCC AAG GCG			1584
48	Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala Val Pro Lys Ala			
49	350	355	360	365
50				
51	TGC TGT GCA CCC ACC AAG CTG AGC GCC ACC TCT GTG CTC TAC TAT GAC			1632
52	Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp			
53	370	375	380	
54				
55	AGC AGC AAC AAC GTC ATC CTG CGC AAA GCC CGC AAC ATG GTG GTC AAG			1680
56	Ser Ser Asn Asn Val Ile Leu Arg Lys Ala Arg Asn Met Val Val Lys			
57	385	390	395	
58				

Interference No. 105,508 (RES)

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1 GCC TGC GGC TGC CAC T GAGTCAGCCC GCCCAGCCCT ACTGCAG  
2 Ala Cys Gly Cys His  
3 400

1723

Dated: October 20, 2006

/CONNIE WONG/

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